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	#11 Search per AND sp	ores AND quantitat*	13:53:16	45
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	#4 Search cruz-perez	[au] and buttner [au]	13:42:36	<u>0</u>
	#3 Search cruz-perez[	au] and buttner[au]	13:42:17	<u>0</u>
	#1 Search cruz-perez	[au] and chartarum	13:28:41	1

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Reverse complemented strand Features: SNP CDD F

1: AF081469. Reports Stachybotrys char...[gi:3420911]

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LOCUS AF081469 936 bp DNA linear PLN 11-JUN-1999

Stachybotrys chartarum strain UAMH 7900 18S ribosomal RNA gene, DEFINITION

partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S

FATCGGATC CCCGG

Structure

History

ribosomal RNA gene, partial sequence.

ACCESSION AF081469

AF081469.1 GI:3420911 VERSION KEYWORDS

SOURCE

Stachybotrys chartarum ORGANISM Stachybotrys chartarum

Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE (bases 1 to 936)

**AUTHORS** Haugland, R.A. and Heckman, J.L.

Identification of putative sequence specific PCR primers for TITLE

detection of the toxigenic fungal species Stachybotrys chartarum

Mol. Cell. Probes 12 (6), 387-396 (1998) JOURNAL

PUBMED 9843656

REFERENCE (bases 1 to 936) 2

Haugland, R.A. and Heckman, J.L. **AUTHORS** 

TITLE Direct Submission

Submitted (30-JUL-1998) Microbiological & Chemical Exposure **JOURNAL** 

Assessment Research Division, National Exposure Research

Laboratory, U.S. Environmental Protection Agency, 26 W. Martin

Luther King Dr., Cincinnati, OH 45268, USA

**FEATURES** Location/Qualifiers

> source 1..936

> > organism="Stachybotrys chartarum"

/mol type="genomic DNA" /strain="UAMH 7900" /db xref="taxon:74722" /tissue\_type="mycelia"

rRNA <1..361

/product="18S ribosomal RNA"

misc RNA 362..520

/product="internal transcribed spacer 1"

/note="ITS1"

rRNA 521..677

/product="5.8S ribosomal RNA"

misc RNA 678..855

/product="internal transcribed spacer 2"

/note="ITS2"

rRNA 856..>936

/product="28S ribosomal RNA"

ORIGIN

1 ccttagatgt cctgggctgc acgcgcgtta cactgacgga gccagcgagt acttccttgt

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121 ttgctcttca acgaggaatc cctagtaagc gcaagtcatc agcttgcgtt gattacgtcc

181 ctgccctttg tacacaccgc ccgtcgctac taccgattga atggcttagt gaggcgttcg

241 gactggtcca gggaggtggg caactaccac ccaggaccgg aaagttctcc aaacttggtc

301 atttagagga agtaaaagtc gtaacaaggt ctccgttggt gaaccagcgg agggatcatt

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